

Figure 1

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Figure 2C

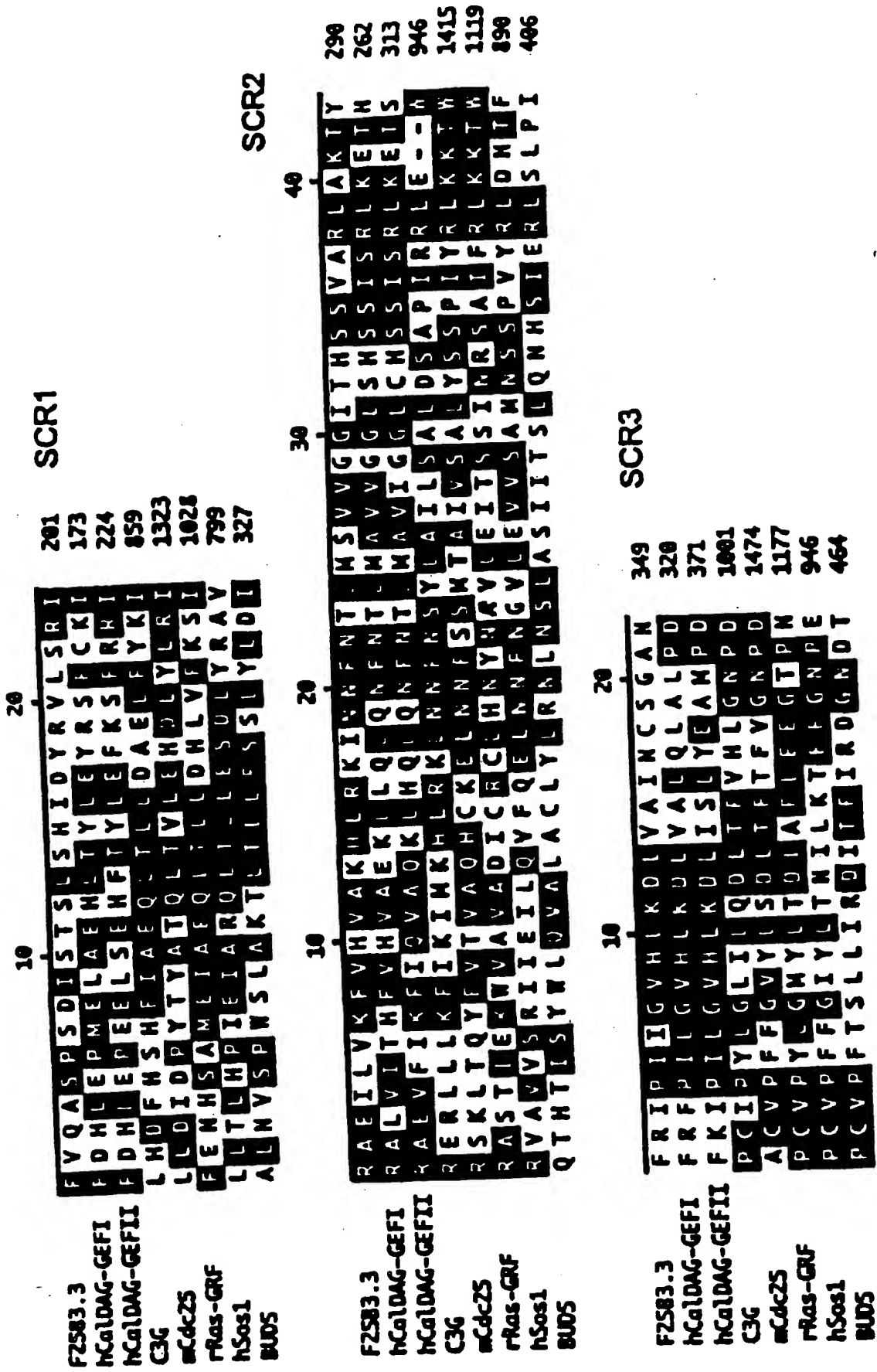


Figure 2A

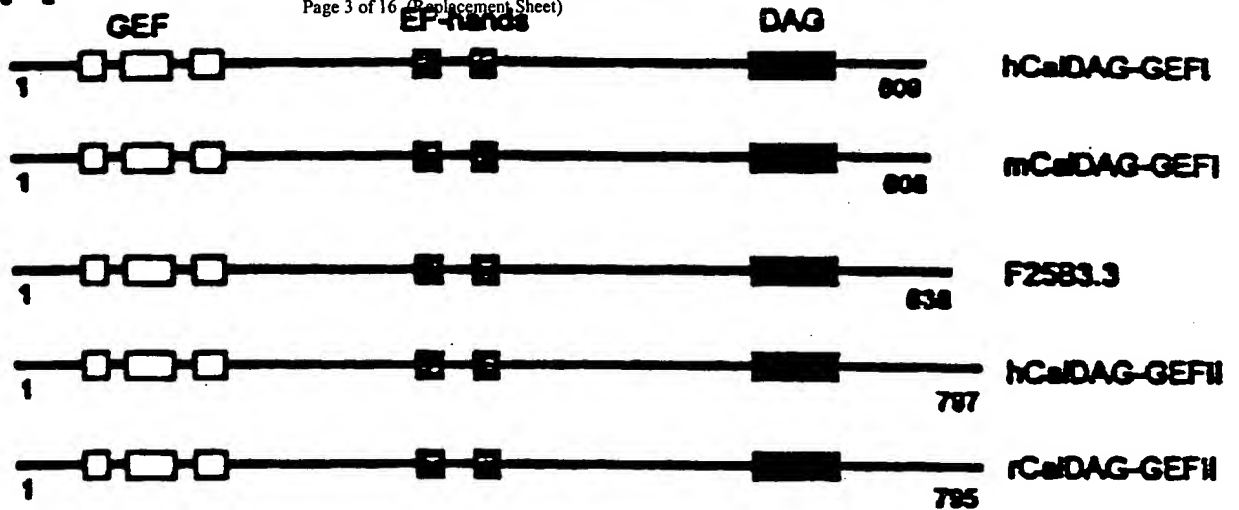


Figure 2B

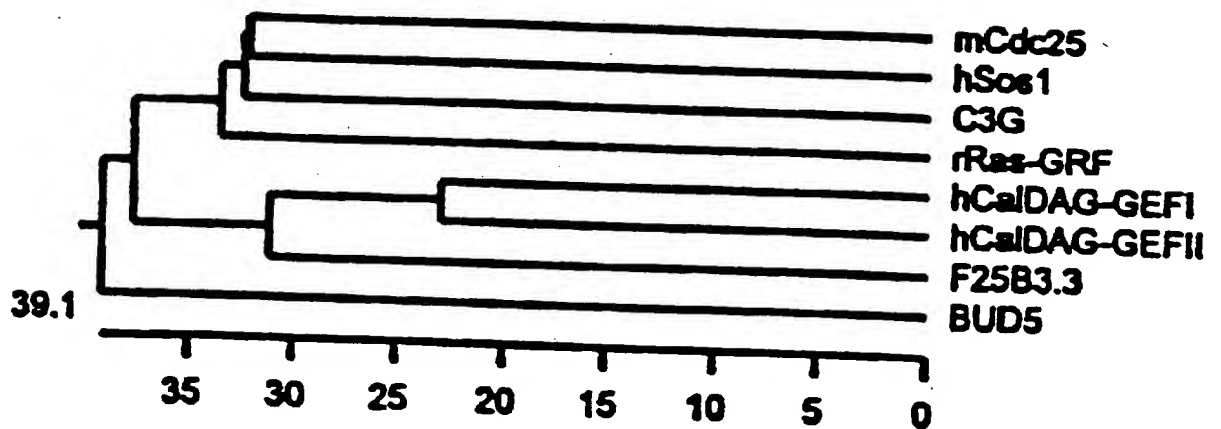


Figure 2D-1

hCaldag-GEFI	M	A	G	T	L	D	L	O	K	G	C	T	V	E	E	L	L	R	G	C	I	E	A	F	D	D	S	G	K	V	R	D	P	Q	L	V	R	M	F	L	M	H	P	M	I	P	S	S		
mCaldag-GEFI	M	A	G	T	L	D	L	O	K	G	C	T	V	E	E	L	L	R	G	C	I	E	A	F	D	D	S	G	K	V	R	D	P	Q	L	V	R	M	F	L	M	H	P	M	I	P	S	S		
hCaldag-GEFI	K	E	L	K	A	L	L	D	Q	E	G	N	R	R	N	S	S	L	I	D	I	S	V	P	T	Y	K	K	R	Q	V	T	Q	R	N	P	V	G	Q	K	K	K	M	S	L	L	F			
mCaldag-GEFI	K	E	L	K	A	L	L	D	Q	E	G	N	R	R	N	S	S	L	I	D	I	S	V	P	T	Y	K	K	R	Q	V	T	Q	R	N	P	V	G	Q	K	K	K	M	S	L	L	F			
hCaldag-GEFI	M	S	V	S	Q	V	Q	L	M	I	L	S	K	P	T	A	P	Q	R	A	L	V	I	T	N	F	V	M	V	A	E	K	L	L	Q	L	Q	N	F	N	T	L	M	A	V	V	G	L		
mCaldag-GEFI	M	S	V	S	Q	V	Q	L	M	I	L	S	K	P	T	A	P	Q	R	A	L	V	I	T	N	F	V	M	V	A	E	K	L	L	Q	L	Q	N	F	N	T	L	M	A	V	V	G	L		
hCaldag-GEFI	F	P	I	L	G	V	N	L	K	D	L	V	A	L	Q	L	A	L	P	D	L	D	P	A	R	T	R	L	N	G	A	K	M	K	Q	L	F	S	I	L	E	E	L	A	M	V	T	S	L	
mCaldag-GEFI	F	P	I	L	G	V	N	L	K	D	L	V	A	L	Q	L	A	L	P	D	L	D	P	A	R	T	R	L	N	G	A	K	M	K	Q	L	F	S	I	L	E	E	L	A	M	V	T	S	L	
hCaldag-GEFI	P	P	R	P	P	V	L	E	E	N	T	S	A	A	K	P	K	L	D	Q	A	L	V	V	E	N	I	E	K	M	V	E	S	V	F	R	N	F	D	V	D	G	D	G	N	I	S	Q	E	E
mCaldag-GEFI	P	P	R	P	P	V	L	E	E	N	T	S	A	A	K	P	K	L	D	Q	A	L	V	V	E	N	I	E	K	M	V	E	S	V	F	R	N	F	D	V	D	G	D	G	N	I	S	Q	E	E
hCaldag-GEFI	F	Q	E	S	N	S	L	R	P	V	A	C	R	N	C	K	A	L	I	L	G	I	Y	K	Q	G	L	K	C	R	A	C	G	V	N	C	N	K	Q	C	K	D	R	L	S	V	E	C	R	
mCaldag-GEFI	F	Q	E	S	N	S	L	R	P	V	A	C	R	N	C	K	A	L	I	L	G	I	Y	K	Q	G	L	K	C	R	A	C	G	V	N	C	N	K	Q	C	K	D	R	L	S	V	E	C	R	
hCaldag-GEFI	E	D	G	V	F	D	I	N	L																																									
mCaldag-GEFI	E	D	G	V	F	D	I	N	L																																									

Figure 2D-2

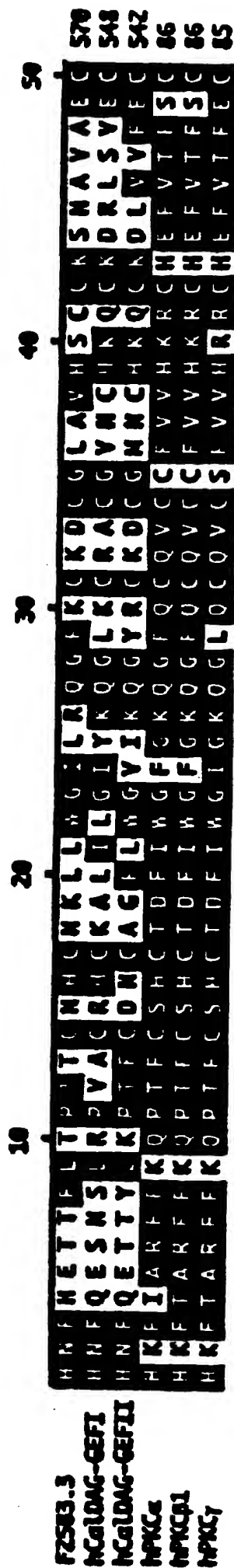
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QLA	KLLN	IYQQSR	KDN	SN	SL	QV	K	T	C	N	L	V	R	Y	N	I	S	A	F	P	A	E	F	D	L	N	P	E	L	A	E	2									
DNLEP	MELAE	NLT	TY	LE	Y	R	S	F	C	K	I	L	F	Q	D	Y	N	S	F	V	T	M	G	C	T	V	D	M	P	V	L	E	R	F	I	S	L	F	300		
DNLEP	MELAE	NLT	TY	LE	Y	R	S	F	C	K	I	L	F	Q	D	Y	N	S	F	V	T	M	G	C	T	V	D	M	P	V	L	E	R	F	I	S	L	F	300		
SNSSIS	RLKET	NS	VS	P	E	T	I	K	L	N	E	G	L	T	E	L	V	T	A	T	G	N	Y	G	N	Y	R	R	R	L	A	C	V	G	F	R	300				
SNSSIS	RLKET	NS	VS	P	E	T	I	K	L	N	E	G	L	T	E	L	V	T	A	T	G	N	Y	G	N	Y	R	R	R	L	A	C	V	G	F	R	300				
RPPVQ	AMPDL	LS	LT	VS	LD	Q	Y	Q	T	E	D	E	L	Y	Q	L	S	L	Q	R	E	P	R	S	K	S	S	P	T	S	P	T	S	C	T	P	400				
RPPVQ	AMPDL	LS	LT	VS	LD	Q	Y	Q	T	E	D	E	L	Y	Q	L	S	L	Q	R	E	P	R	S	K	S	S	P	T	S	P	T	S	C	T	P	400				
FQIIR	GNFP	YLS	AF	GL	LD	Q	N	Q	Q	C	I	S	R	E	E	N	S	Y	F	L	R	S	S	S	V	L	G	G	R	M	G	F	V	N	500						
FQIIR	GNFP	YLS	AF	GL	LD	Q	N	Q	Q	C	I	S	R	E	E	N	S	Y	F	L	R	S	S	S	V	L	G	G	R	M	G	F	V	N	500						
RAQS	VSL	EG	S	A	P	S	P	S	P	M	N	S	H	N	R	A	F	S	F	S	L	P	R	P	C	R	G	S	R	P	P	E	I	R	E	E	V	Q	T	V	600
RAQS	VSL	EG	S	A	P	S	P	S	P	M	N	S	H	N	R	A	F	S	F	S	L	P	R	P	C	R	G	S	R	P	P	E	I	R	E	E	V	Q	T	V	600

Figure 2E

F2S3.3
 hCalDAG-GEFI
 hCalDAG-GEFII
 hCalmodulin
 hCalbindin D28K
 hCalctonurin B
 hParvalbumin α
 hTropomyosin C

	10										20									
A	V	F	K	N	H	Y	D	H	D	R	D	G	F	L	S	V	L	F	Q	473
S	V	F	R	N	T	D	V	D	G	D	G	D	G	H	I	S	Q	E	F	452
S	V	F	K	N	Y	D	H	D	Q	D	G	D	G	Y	I	S	Q	E	F	447
E	A	I	S	L	F	D	K	D	G	D	G	D	G	T	I	T	T	K	L	34
L	M	L	K	L	F	D	S	N	H	D	G	D	G	K	L	E	L	T	E	163
F	A	F	R	I	Y	D	H	D	K	D	G	D	G	Y	I	S	N	G	E	113
K	V	F	H	M	L	D	K	D	K	S	C	F	I	E	E	D	E	L	Q	65
E	C	E	R	I	F	D	R	N	A	D	G	D	G	Y	I	D	P	E	E	117

Figure 2F



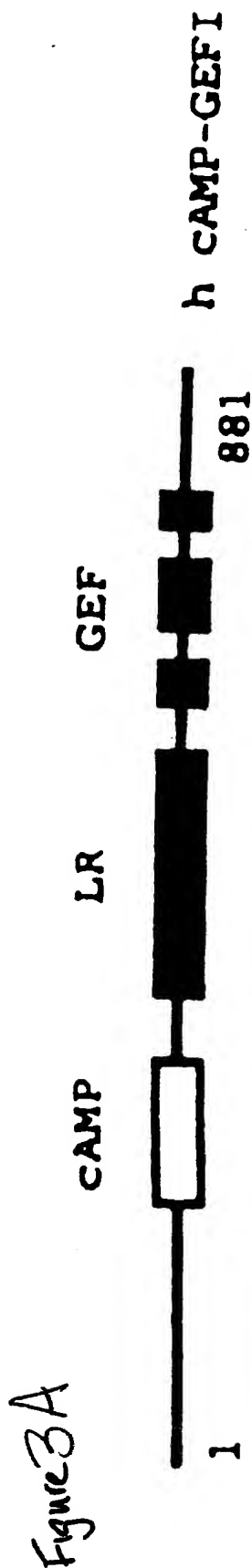


Figure
3B

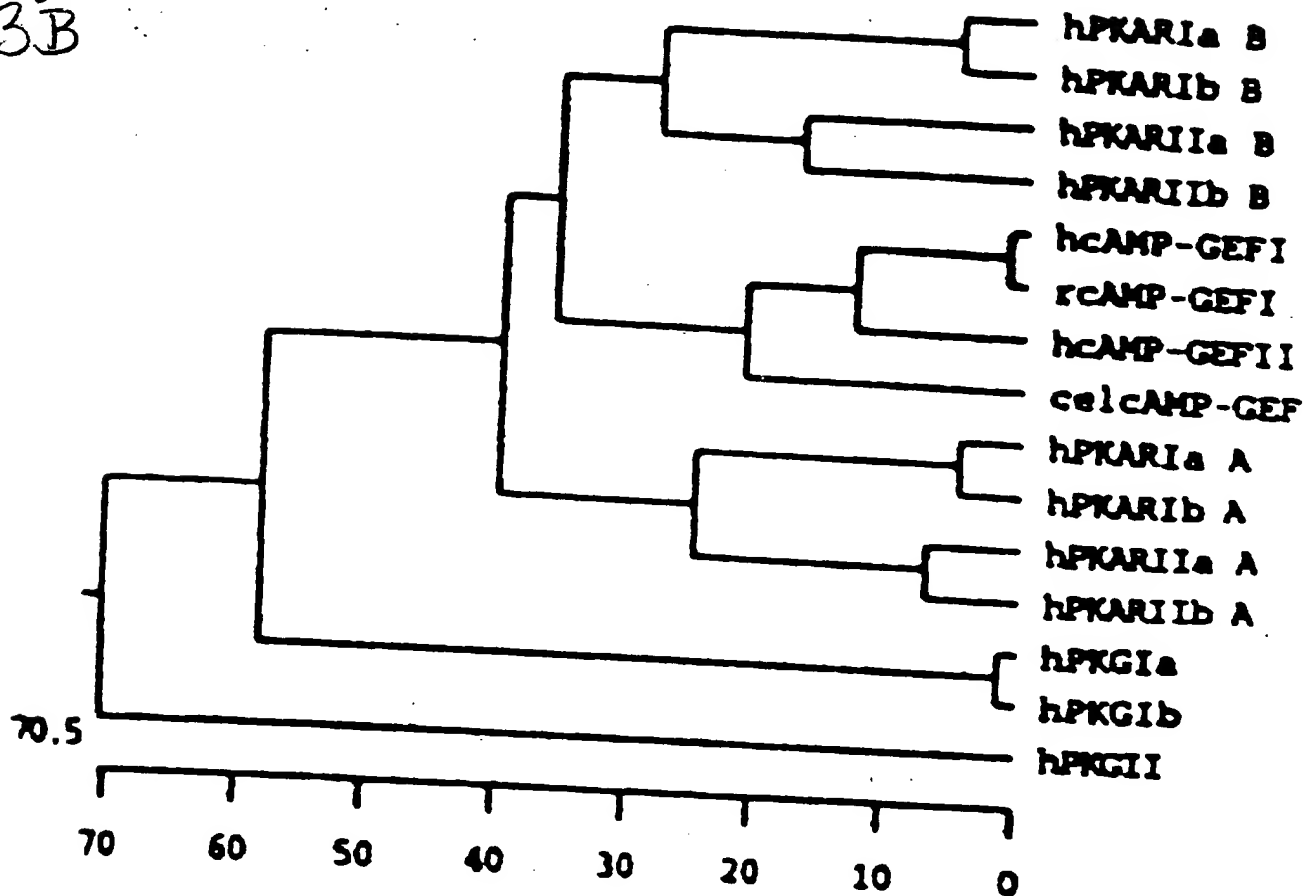


Figure 3C

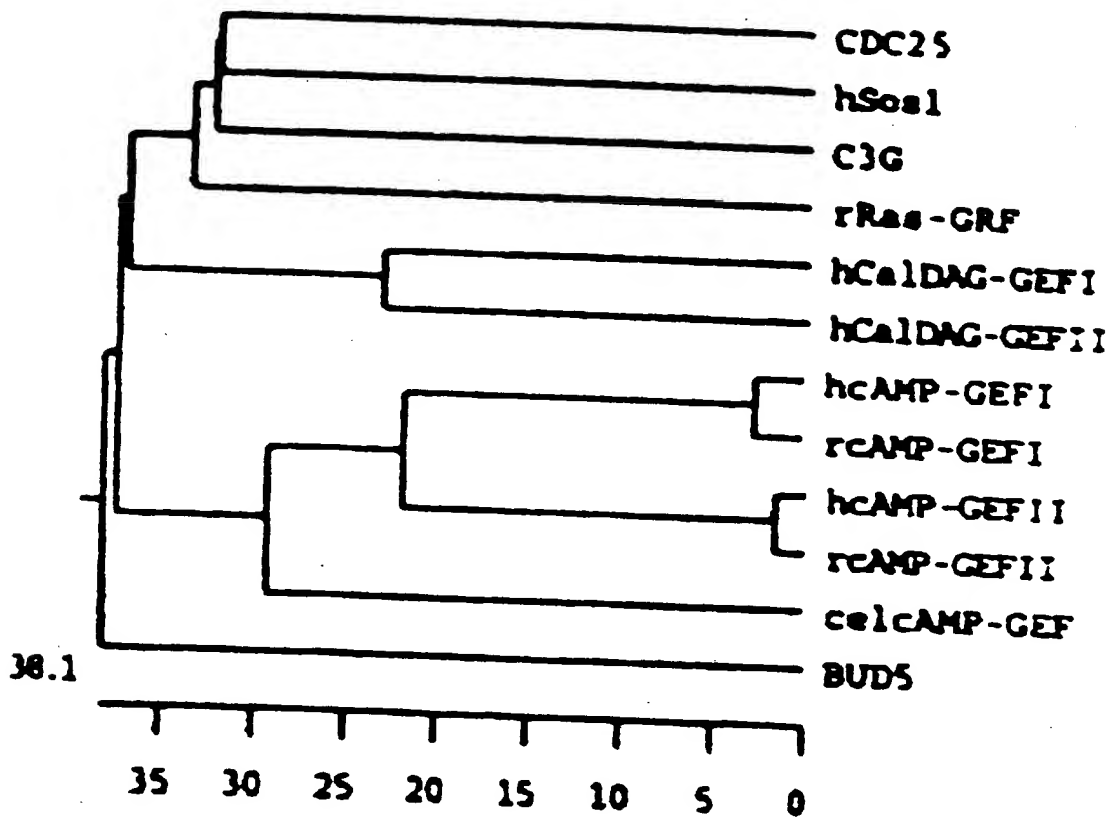


Figure
 3D-1

hCAMP-GEFI	L	D	L	V	S	A	K	D	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	639	
hCAMP-GEFI	L	D	L	V	S	A	K	D	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	642	
hCAMP-GEFII	F	E	L	M	S	S	K	D	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	791	
hCAMP-GEFII	F	E	L	M	S	S	K	D	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	216	
celCAMP-GEF	L	E	L	I	D	S	Q	E	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	1010	
hCa12DAG-GEFI	F	D	E	L	E	P	M	E	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	173	
hCa12DAG-GEFII	F	D	E	L	E	P	M	E	L	A	G	Q	L	T	D	E	D	W	L	F	N	S	I	224	
C3G	L	E	D	F	E	S	M	E	I	A	E	Q	L	T	L	D	E	D	W	L	F	N	S	I	859
CDC25	L	L	D	I	D	P	M	E	I	A	E	Q	L	T	L	D	E	D	W	L	F	N	S	I	1323
hRas-GRF	F	E	E	M	S	A	M	E	I	A	E	Q	L	T	L	D	E	D	W	L	F	N	S	I	1028
hSos1	L	L	T	L	M	P	I	E	I	A	E	Q	L	T	L	D	E	D	W	L	F	N	S	I	799
BUD5	A	L	M	V	S	P	M	S	L	A	K	T	L	T	L	L	E	S	S	L	Y	L	D	I	327

Figure 3D-3

SCR 3										10	20												
731	P	V	I	P	P	M	P	L	L	L	K	D	M	T	F	I	H	E	G	N	T	789	
734	P	V	I	P	P	M	P	L	L	L	K	D	M	T	F	I	H	E	G	N	T	792	
882	P	L	I	P	P	M	P	L	L	L	K	D	M	T	F	I	H	E	G	N	T	940	
307	P	L	I	P	P	M	P	L	L	L	K	D	M	T	F	I	H	E	G	N	T	365	
1101	P	Y	I	P	P	V	P	L	I	L	K	D	L	M	P	I	H	Q	G	N	K	S	1159
262	P	R	P	P	I	L	G	V	E	L	K	D	L	V	A	L	Q	L	A	L	P	D	320
313	P	K	I	P	I	L	G	V	E	L	K	D	L	I	S	L	Y	E	A	M	P	D	371
946	P	C	I	P	Y	L	G	L	I	L	Q	D	L	T	P	V	H	L	G	N	P	D	1001
1415	A	C	V	P	F	P	G	V	Y	L	S	D	L	T	F	T	V	G	N	P	D	1474	
1119	P	C	V	P	Y	L	G	M	Y	L	T	D	L	A	F	L	E	C	T	P	M	1177	
890	P	C	V	P	P	P	G	I	Y	L	T	M	I	L	K	T	E	E	G	N	P	E	946
406	P	C	V	P	P	T	S	L	L	I	R	D	I	T	F	I	R	D	C	N	D	T	464

Figure 3E-1

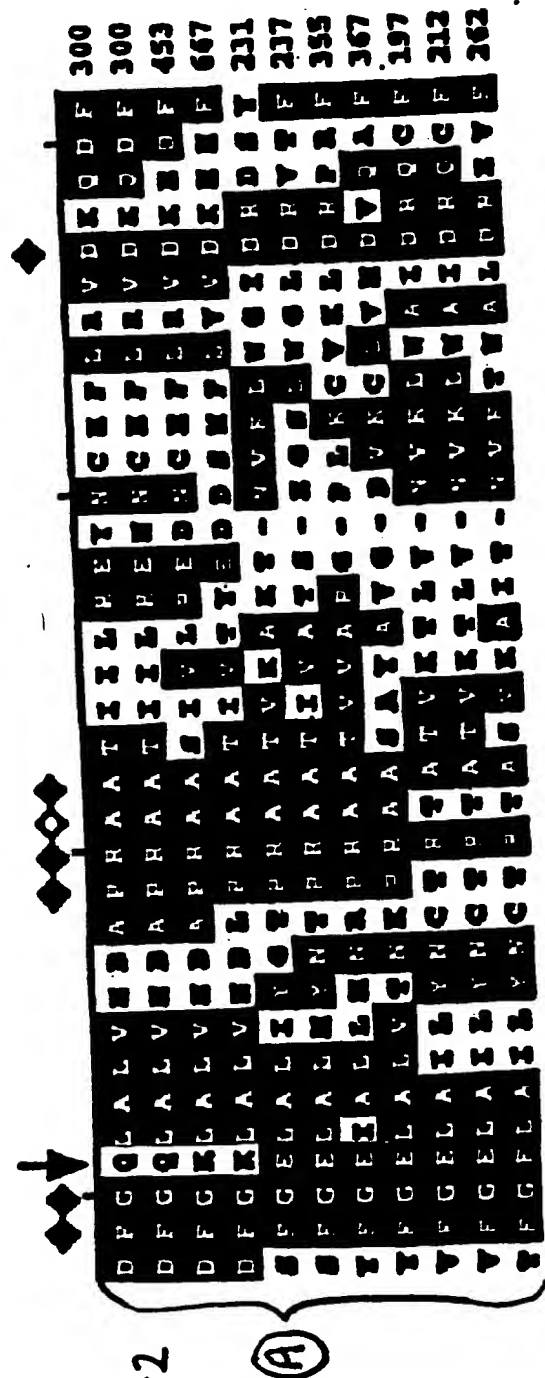
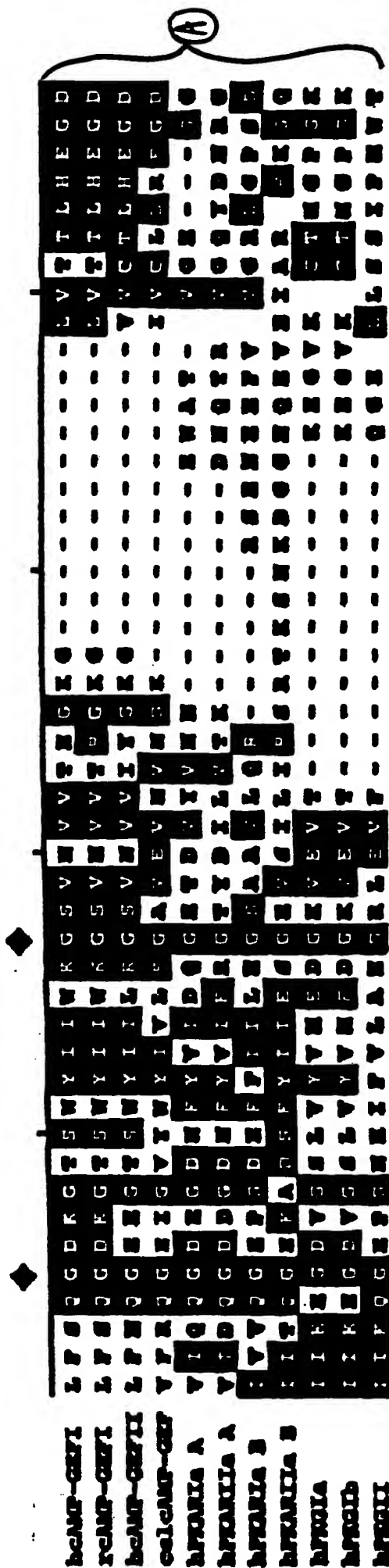


Figure 3E-2

Figure 3 F-1

bcAMP-GEFI	NVL-----	RRNRPR-----
bcAMP-GEFII	NVAAHAANSSSSAEWIACLDERPLERSSESDVDIIFTR	
bcAMP-GEFI	-----	HQHPSCIQ-----
bcAMP-GEFII	YAVLAGSLDVKVSETSSHQDAVTICTLCIGTAFGRSI	
bcAMP-GEFI	-----	TPLTNSSESLDPSESLERQ
bcAMP-GEFII	PYGVNETGSHNDRIIPDKENTPLIEPHVPLRPANTITR	
bcAMP-GEFI	LVDGILALGLGVNSRSQVVGICQVLLDEGALCHVKND	
bcAMP-GEFII	LVDWNNHQQTFCVNSRTQAVGNWQVLLLEDGVLEHVDQR	
bcAMP-GEFI	SQRGPDALLTVALRKPPGQRTDEELDLIFRELLNIKA	
bcAMP-GEFII	SQNGPDANNNMILRKPPGQRTVDDLEIIFYRELLNIKA	
bcAMP-GEFI	GSVHVVTGKGLVTTLEHGDDFGQLALVNDAPRAATI	
bcAMP-GEFII	GSVHVVIYGKGVVCTLEHGDDFGKLALVNDAPRAASI	
bcAMP-GEFI	ASQGA-GPSRPFTFGNNRYTVNSGTFDKILELLLEAN	
bcAMP-GEFII	VPAGNRASHNQNSQFQQRITVNSGTFDKILEHFLLETI	
bcAMP-GEFI	GSSEQRSTYVCMKRQQILRLVSSQWVALYGSMLHTDP	
bcAMP-GEFII	QGTTEQEKNDYALNNKRRVIRLVLOWAANYGDLLOEDD	
bcAMP-GEFI	SPQNKARNLPVWLPNQDEPLFGSSCAIQVGDKVPYDI	
bcAMP-GEFII	APQKKKHKVLLQQFNTGDER-AQKRQPIRGSDDEVLPKY	
bcAMP-GEFI	GDAIGLQPDARGVATSLGLNERLFVVNPFQEVNELIPH	
bcAMP-GEFII	GEXVVLKPNDSVFTTLTINGRLFACPREQFDSLTPL	
bcAMP-GEFI	HYVLGPQHLRDVTTANLERFNRREFNELQYMWATELCCL	
bcAMP-GEFII	YNTFGRRNFKK-TTANLDLFLRRRFNEIQFWVVTETICL	
bcAMP-GEFI	RLAHTWERLPHKVRKLYSALERLLDPSENNRVYRLAL	
bcAMP-GEFII	RLALTWEKLPSEKFKFYAEFESLNDPSERNRDAYRLTV	
bcAMP-GEFI	AARMNLNCRSHNPVFLSPFLRRRVSHLNEDSQVARIST	
bcAMP-GEFII	TARTVRYYSQ---PFNF-----	

Figure 3F-2

LKEVKAFKFKFNLNQLCLCSYQLLE 20
 LCGYENLEKGITLFRQGDIGTNW 80
 LDNTPRNATIVTRESSELRLRIEQKDFKALWEEKYROYNAGLLAP 32
 160
 ASTERVLRAGRQLNQHLATCFNLIRDRKYNLRLYRQCCSGRE 92
 VPSEKILRAGKILRNAILSRAPENIRDRKYNLKTYRQCCVGT 240
 WAFQDRDAQFYRFPGPEPE--PVGTHEN--EELAEAVALL 166
 HNFQDK-YLFYRFLDDENEDAPLPTRERKKKCDDEELQDTHLL 319
 VANLSNENVERRELAVALFEPHSEKAGTVLFSQGDKGTSNYIINK 246
 LSHLSSTTVRERELAGVLIPESEHAKGCTVLFNQGEKTSNYIILK 399
 ILREYNCHNPLRVDEKQDFNRILKDVRAKTNRLLENKGVVLVLER 326
 VLREDNCHNPLRVDEKQDFNRILRDVEANTVRLKENDDQDVLVLEK 479
 GLDSSANDPKETFLSDFLLTHERVFNPSAQLCALLENHFNVEPA 405
 RLKATLNKATDSVLNDFINNHCVFNPNHTQLCPALVANTHAQPS 559
 VATSFLHKLSDLVGRDTRLSENLLRQWPERRRRCHRLNCGGNA 485
 VSKAFLEEFYVEVSDDARNIAALKRQLPELEKIVKQISE-DAK 638
 CRPDNSVLTTLQLPVTASVREVMAALAQEDGWTEKGQVLVKVNSA 565
 YCHNDHTYTTIRVPVATSVKEVISAVADKLGSGEGLIIVKNSG 717
 PDQLGPTVGSAEGLDLVSAKDLAGQLTDNDWSLFNSHQVELI 645
 PEQEGPTVGTVGTFLNLSKDLATQNTIYDWELEFCVHELELI 797
 CPVPGPRAQLLKKFKILAAHLKEQKENVNSFFAVNFGLENSPIS 725
 CSQLSKRVQLLKKFKILAAHCKEYKENVNSFFAIVNGLSNIAVS 876
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